

**WHAT IS CLAIMED IS:**

1. An isolated nucleic acid comprising a sequence that encodes a polypeptide having alpha amylase activity, wherein said sequence is selected from the group consisting of:  
SEQ ID NO:1;  
variants having at least about 50% homology to at least one of SEQ ID NO:1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;  
sequences complementary to SEQ ID NO:1; and  
sequences complementary to variants having at least about 50% homology to SEQ ID NO:1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection.
2. The isolated nucleic acid as claimed in claim 1, wherein the isolated nucleic acid comprises a complementary sequence that hybridizes under conditions of high stringency to a sequence selected from the group consisting of: SEQ ID NO:1, and variants having at least about 50% homology to at least one of SEQ ID NO:1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection.
3. The isolated nucleic acid as claimed in claim 1, wherein the isolated nucleic acid comprises a complementary sequence that hybridizes under conditions of moderate stringency to a sequence selected from the group consisting of: SEQ ID NO:1, and variants having at least about 50% homology to at least one of SEQ ID NO:1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection.
4. The isolated nucleic acid as claimed in claim 1, wherein the isolated nucleic acid comprises a complementary sequence that hybridizes under conditions of low stringency to a sequence selected from the group consisting of: SEQ ID NO:1, and variants having at least about 50%

5. The isolated nucleic acid as claimed in claim 1, wherein said variants have at least about 50% homology to at least one of SEQ ID NO:1, over a region of at least about 200 residues, as determined by analysis with a sequence comparison algorithm.
6. The isolated nucleic acid according to claim 1, wherein said variants have at least about 50% homology to at least one of SEQ ID NO:1 over the entire sequence.
7. The isolated nucleic acid according to claim 1, 2, 3, 4, 5 or 6, wherein said variants have at least about 55% homology to at least one of SEQ ID NO:1.
8. The isolated nucleic acid according to claim 1, 2, 3, 4, 5 or 6, wherein said variants have at least about 60% homology to at least one of SEQ ID NO:1.
9. The isolated nucleic acid according to claim 1, 2, 3, 4, 5 or 6, wherein said variants have at least about 65% homology to at least one of SEQ ID NO:1.
10. The isolated nucleic acid according to claim 1, 2, 3, 4, 5 or 6, wherein said variants have at least about 70% homology to at least one of SEQ ID NO:1.
11. The isolated nucleic acid according to claim 1, 2, 3, 4, 5 or 6, wherein said variants have at least about 75% homology to at least one of SEQ ID NO:1.
12. The isolated nucleic acid according to claim 1, 2, 3, 4, 5 or 6, wherein said variants have at least about 80% homology to at least one of SEQ ID NO:1.
13. The isolated nucleic acid according to claim 1, 2, 3, 4, 5 or 6, wherein said variants have at least about 85% homology to at least one of SEQ ID NO:1.



20. The isolated nucleic acid as claimed in claim 17, 18 or 19, wherein said sequence has at least about 55% homology to a sequence selected from the group consisting of SEQ ID NO:1.
21. The isolated nucleic acid as claimed in claim 17, 18 or 19, wherein said sequence has at least about 60% homology to a sequence selected from the group consisting of SEQ ID NO:1.
22. The isolated nucleic acid as claimed in claim 17, 18 or 19, wherein said sequence has at least about 65% homology to a sequence selected from the group consisting of SEQ ID NO:1.
23. The isolated nucleic acid as claimed in claim 17, 18 or 19, wherein said sequence has at least about 70% homology to a sequence selected from the group consisting of SEQ ID NO:1.
24. The isolated nucleic acid as claimed in claim 17, 18 or 19, wherein said sequence has at least about 75% homology to a sequence selected from the group consisting of SEQ ID NO:1.
25. The isolated nucleic acid as claimed in claim 17, 18 or 19, wherein said sequence has at least about 80% homology to a sequence selected from the group consisting of SEQ ID NO:1.
26. The isolated nucleic acid as claimed in claim 17, 18 or 19, wherein said sequence has at least about 85% homology to a sequence selected from the group consisting of SEQ ID NO:1.
27. The isolated nucleic acid as claimed in claim 17, 18 or 19, wherein said sequence has at least about 90% homology to a sequence selected from the group consisting of SEQ ID NO:1.
28. The isolated nucleic acid as claimed in claim 17, 18 or 19, wherein said sequence has at least about 95% homology to a sequence selected from the group consisting of SEQ ID NO:1.
29. An isolated nucleic acid encoding a polypeptide selected from the group consisting of:  
polypeptides having an amino acid sequence selected from the group consisting of:  
SEQ ID NO:2;

variants having at least about 50% homology to at least one of SEQ ID NO:2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;  
sequences complementary to SEQ ID NO:2; and  
sequences complementary to variants having at least about 50% homology to SEQ ID NO:2 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and  
polypeptides having at least 10 consecutive amino acids of a polypeptide having a sequence selected from the group consisting of SEQ ID NO:2.

30. A purified polypeptide selected from the group consisting of:  
polypeptides having an amino acid sequence selected from the group consisting of: SEQ ID NO:2;

variants having at least about 50% homology to at least one of SEQ ID NO:2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;  
sequences complementary to SEQ ID NO:2; and  
sequences complementary to variants having at least about 50% homology to SEQ ID NO:2 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and  
polypeptides having at least 10 consecutive amino acids of a polypeptide having a sequence selected from the group consisting of SEQ ID NO:2.

31. The purified polypeptide as claimed in claim 30, wherein the amino acid sequence has at least about 50% homology to a sequence selected from the group consisting of SEQ ID NO:2, over a region of at least about 200 residues.

32. The purified polypeptide as claimed in claim 30, wherein the amino acid sequence has at least about 50% homology to a sequence selected from the group consisting of SEQ ID NO:2, over the entire sequence.

33. The purified polypeptide as claimed in claim 30, 31 or 32, wherein in the amino acid sequence has at least about 55% homology to a sequence selected from the group consisting of SEQ ID NO:2.
34. The purified polypeptide as claimed in claim 30, 31 or 32, wherein the amino acid sequence has at least about 60% homology to a sequence selected from the group consisting of SEQ ID NO:2.
35. The purified polypeptide as claimed in claim 30, 31 or 32, wherein the amino acid sequence has at least about 65% homology to a sequence selected from the group consisting of SEQ ID NO:2.
36. The purified polypeptide as claimed in claim 30, 31 or 32, wherein the amino acid sequence has at least about 70% homology to a sequence selected from the group consisting of SEQ ID NO:2.
37. The purified polypeptide as claimed in claim 30, 31 or 32, wherein the amino acid sequence has at least about 75% homology to a sequence selected from the group consisting of SEQ ID NO:2.
38. The purified polypeptide as claimed in claim 30, 31 or 32, wherein the amino acid sequence has at least about 80% homology to a sequence selected from the group consisting of SEQ ID NO:2.
39. The purified polypeptide as claimed in claim 30, 31 or 32, wherein the amino acid sequence has at least about 85% homology to a sequence selected from the group consisting of SEQ ID NO:2.

40. The purified polypeptide as claimed in claim 30, 31 or 32, wherein the amino acid sequence has at least about 90% homology to a sequence selected from the group consisting of SEQ ID NO:2.
41. The purified polypeptide as claimed in claim 30, 31 or 32, wherein the amino acid sequence has at least about 95% homology to a sequence selected from the group consisting of SEQ ID NO:2.
42. A purified polypeptide as claimed in claim 30, having an amino acid sequence selected from the group consisting of SEQ ID NO:2; and sequences having at least about 50% homology to at least one of SEQ ID NO:2, over the entire sequence.
43. A purified antibody that specifically binds to a polypeptide selected from the group consisting of:  
polypeptides comprising an amino acid sequence selected from the group consisting of:  
SEQ ID NO:2;  
variants having at least about 50% homology to at least one of SEQ ID NO:2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;  
sequences complementary to SEQ ID NO:2; and  
sequences complementary to variants having at least about 50% homology to SEQ ID NO:2 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and  
polypeptides having at least 10 consecutive amino acids of a polypeptide having a sequence selected from the group consisting of SEQ ID NO:2.
44. A purified antibody as claimed in claim 43, that specifically binds to a polypeptide having at least 10 consecutive amino acids of a polypeptide selected from the group consisting of SEQ ID NO:2.

45. The antibody of claim 43, wherein the antibodies are polyclonal.
46. The antibody of claim 43, wherein the antibodies are monoclonal.
47. A method of producing a polypeptide selected from the group consisting of:  
polypeptides having an amino acid sequence selected from the group consisting of: SEQ ID NO:2;  
variants having at least about 50% homology to at least one of SEQ ID NO:2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;  
sequences complementary to SEQ ID NO:2; and  
sequences complementary to variants having at least about 50% homology to SEQ ID NO:2 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and  
polypeptides having at least 10 consecutive amino acids of a polypeptide having a sequence selected from the group consisting of SEQ ID NO:2; comprising the steps of introducing a nucleic acid encoding the polypeptide into a host cell under conditions that allow expression of the polypeptide, and recovering the polypeptide.
48. A method of producing a polypeptide comprising at least 10 amino acids of a sequence selected from the group consisting of SEQ ID NO:2, comprising the steps of: introducing a nucleic acid encoding the polypeptide, operably linked to a promoter, into a host cell under conditions that allow expression of the polypeptide, and recovering the polypeptide.
49. A method of generating a variant comprising:  
obtaining a nucleic acid comprising a polynucleotide selected from the group consisting of:  
SEQ ID NO:1;

variants having at least about 50% homology to at least one of SEQ ID NO:1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;

sequences complementary to SEQ ID NO:1; and

sequences complementary to variants having at least about 50% homology to SEQ ID NO:1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and

fragments comprising at least 30 consecutive nucleotides any of the foregoing sequences; and

modifying one or more nucleotides in said polynucleotide to another nucleotide, deleting one or more nucleotides in said polynucleotide, or adding one or more nucleotides to said polynucleotide.

50. The method of claim 49, wherein the modifications are introduced by a method selected from the group consisting of: error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis and any combination of these methods.
51. The method of claim 50, wherein the modifications are introduced by error-prone PCR.
52. The method of claim 50, wherein the modifications are introduced by shuffling.
53. The method of claim 50, wherein the modifications are introduced by oligonucleotide-directed mutagenesis.
54. The method of claim 50, wherein the modifications are introduced by assembly PCR.

55. The method of claim 50, wherein the modifications are introduced by sexual PCR mutagenesis.
56. The method of claim 50, wherein the modifications are introduced by *in vivo* mutagenesis.
57. The method of claim 50, wherein the modifications are introduced by cassette mutagenesis.
58. The method of claim 50, wherein the modifications are introduced by recursive ensemble mutagenesis.
59. The method of claim 50, wherein the modifications are introduced by exponential ensemble mutagenesis.
60. The method of claim 50, wherein the modifications are introduced by site-specific mutagenesis.
61. The method of claim 50, wherein the modifications are introduced by gene reassembly.
62. The method of claim 50, wherein the modifications are introduced by gene site saturated mutagenesis.
63. A computer readable medium having stored thereon a sequence selected from the group consisting of:
- nucleic acid sequences of SEQ ID NO:1;
  - variants of a nucleic acid sequence having at least about 50% homology to at least one of SEQ ID NO:1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;
  - nucleic acid sequences complementary to SEQ ID NO:1;
  - nucleic acid sequences complementary to variants of nucleic acid sequences having at least about 50% homology to SEQ ID NO:1 over a region of at least about 100

residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;

polypeptide sequences SEQ ID NO:2;

variants of polypeptide sequences having at least about 50% homology to at least one of SEQ ID NO:2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;

polypeptide sequences complementary to SEQ ID NO:2; and

polypeptide sequences complementary to variants of polypeptide sequences having at least about 50% homology to SEQ ID NO:2 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection.

64. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a sequence selected from the group consisting of:

nucleic acid sequences of SEQ ID NO:1;

variants of a nucleic acid sequence having at least about 50% homology to at least one of SEQ ID NO:1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;

nucleic acid sequences complementary to SEQ ID NO:1;

nucleic acid sequences complementary to variants of nucleic acid sequences having at least about 50% homology to SEQ ID NO:1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;

polypeptide sequences SEQ ID NO:2;

variants of polypeptide sequences having at least about 50% homology to at least one of SEQ ID NO:2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;

polypeptide sequences complementary to SEQ ID NO:2; and

polypeptide sequences complementary to variants of polypeptide sequences having at least about 50% homology to SEQ ID NO:2 over a region of at least about 100

residues, as determined by analysis with a sequence comparison algorithm or by visual inspection.

65. The computer system of claim 64, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.
66. The computer system of claim 65, wherein the sequence comparison algorithm comprises a computer program which indicates polymorphisms.
67. The computer system of claim 64, further comprising an identifier which identifies one or more features in said sequence.
68. A method for comparing a first sequence to a second sequence comprising the steps of:  
reading the first sequence and the second sequence through use of a computer program which compares sequences; and  
determining differences between the first sequence and the second sequence with the computer program, wherein said first sequence is a sequence selected from the group consisting of:  
nucleic acid sequences of SEQ ID NO:1;  
variants of a nucleic acid sequence having at least about 50% homology to at least one of SEQ ID NO:1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;  
nucleic acid sequences complementary to SEQ ID NO:1;  
nucleic acid sequences complementary to variants of nucleic acid sequences having at least about 50% homology to SEQ ID NO:1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;  
polypeptide sequences SEQ ID NO:2;

variants of polypeptide sequences having at least about 50% homology to at least one of SEQ ID NO:2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;

polypeptide sequences complementary to SEQ ID NO:2; and

polypeptide sequences complementary to variants of polypeptide sequences having at least about 50% homology to SEQ ID NO:2 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection.

69. The method of claim 68, wherein the step of determining differences between the first sequence and the second sequence further comprises the step of identifying polymorphisms.

70. A method for identifying a feature in a sequence comprising the steps of:

reading the sequence using a computer program which identifies one or more features in a sequence; and

identifying one or more features in the sequence with the computer program,

wherein the sequence is selected from the group consisting of:

nucleic acid sequences of SEQ ID NO:1;

variants of a nucleic acid sequence having at least about 50% homology to at least one of SEQ ID NO:1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;

nucleic acid sequences complementary to SEQ ID NO:1;

nucleic acid sequences complementary to variants of nucleic acid sequences having at least about 50% homology to SEQ ID NO:1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;

polypeptide sequences SEQ ID NO:2;

variants of polypeptide sequences having at least about 50% homology to at least one of SEQ ID NO:2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;

polypeptide sequences complementary to SEQ ID NO:2; and  
polypeptide sequences complementary to variants of polypeptide sequences  
having at least about 50% homology to SEQ ID NO:2 over a region of at least about 100  
residues, as determined by analysis with a sequence comparison algorithm or by visual  
inspection.

71. A method of hydrolyzing a starch linkage comprising contacting a substance containing the  
starch with a polypeptide selected from the group consisting of SEQ ID NO:2, and  
sequences substantially identical thereto, under conditions which facilitate the hydrolysis of  
the carbon-halogen linkage.

72. A method of catalyzing the breakdown of a starch, comprising the step of contacting a  
sample containing starch with a polypeptide having a sequence selected from the group  
consisting of:

polypeptide sequences SEQ ID NO:2;  
variants of polypeptide sequences having at least about 50% homology to at least  
one of SEQ ID NO:2, over a region of at least about 100 residues, as determined by  
analysis with a sequence comparison algorithm or by visual inspection;  
polypeptide sequences complementary to SEQ ID NO:2; and  
polypeptide sequences complementary to variants of polypeptide sequences  
having at least about 50% homology to SEQ ID NO:2 over a region of at least about 100  
residues, as determined by analysis with a sequence comparison algorithm or by visual  
inspection;

under conditions which facilitate the breakdown of the haloalkane or halocarboxylic acid.

contacting the polypeptide of SEQ ID NO:2, and sequences having at least about 50% homology to SEQ ID NO:2 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, polypeptide fragments or variants encoded by SEQ ID NO:1, sequences having at least about 50% homology to SEQ ID NO:1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and sequences complementary to any of the foregoing sequences, with a substrate molecule under conditions which allow the particular polypeptide to function; and

detecting either a decrease in an amount of a substrate or an increase in an amount of a reaction product which results from a reaction between said polypeptide and said substrate; wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product is indicative of existence of the functional polypeptide.

74. A nucleic acid probe comprising an oligonucleotide from about 10 to 50 nucleotides in length and having a segment of at least 10 contiguous nucleotides that is at least 50% complementary to a nucleic acid target region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1; and which hybridizes to the nucleic acid target region under moderate to highly stringent conditions to form a detectable target:probe duplex.

75. The probe of claim 74, wherein the oligonucleotide is DNA.

76. The probe of claim 74, wherein the oligonucleotide has a segment of at least 10 contiguous nucleotides that is at least 55% complementary to the nucleic acid target region.

77. The probe of claim 74, wherein the oligonucleotide has a segment of at least 10 contiguous nucleotides that is at least 60% complementary to the nucleic acid target region.
78. The probe of claim 74, wherein the oligonucleotide has a segment of at least 10 contiguous nucleotides that is at least 65% complementary to the nucleic acid target region.
79. The probe of claim 74, wherein the oligonucleotide has a segment of at least 10 contiguous nucleotides that is at least 70% complementary to the nucleic acid target region.
80. The probe of claim 74, wherein the oligonucleotide has a segment of at least 10 contiguous nucleotides that is at least 75% complementary to the nucleic acid target region.
81. The probe of claim 74, wherein the oligonucleotide has a segment of at least 10 contiguous nucleotides that is at least 80% complementary to the nucleic acid target region.
82. The probe of claim 74, wherein the oligonucleotide has a segment of at least 10 contiguous nucleotides that is at least 85% complementary to the nucleic acid target region.
83. The probe of claim 74, wherein the oligonucleotide has a segment of at least 10 contiguous nucleotides that is at least 90% complementary to the nucleic acid target region.
84. The probe of claim 74, wherein the oligonucleotide has a segment of at least 10 contiguous nucleotides that is at least 95% complementary to the nucleic acid target region.
85. The probe of claim 74, wherein the oligonucleotide has a segment of at least 10 contiguous nucleotides that is fully complementary to the nucleic acid target region.
86. The probe of claim 74, wherein the oligonucleotide is 15-50 bases in length.

87. The probe of claim 74, wherein the probe further comprises a detectable isotopic label.
88. The probe of claim 74, wherein the probe further comprises a detectable non-isotopic label selected from the group consisting of a fluorescent molecule, a chemiluminescent molecule, an enzyme, a cofactor, an enzyme substrate, and a hapten.
89. The probe of claim 86, wherein the oligonucleotide has a segment of at least 15 contiguous nucleotides that is at least 90% complementary to the nucleic acid target region, and which hybridizes to the nucleic acid target region under moderate to highly stringent conditions to form a detectable target:probe duplex.
90. The probe of claim 86, wherein the oligonucleotide has a segment of at least 15 contiguous nucleotides that is at least 95% complementary to a nucleic acid target region, and which hybridizes to the nucleic acid target region under moderate to highly stringent conditions to form a detectable target:probe duplex.
91. The probe of claim 86, wherein the oligonucleotide has a segment of at least 15 contiguous nucleotides that is at least 97% complementary to a nucleic acid target region, and which hybridizes to the nucleic acid target region under moderate to highly stringent conditions to form a detectable target:probe duplex.
92. A polynucleotide probe for isolation or identification of alpha amylase genes having a sequence which is the same as, or fully complementary to at least a fragment of one of SEQ ID NO:1.
93. A protein preparation comprising a polypeptide selected from the group consisting of: polypeptides having an amino acid sequence selected from the group consisting of:  
SEQ ID NO:2;

variants having at least about 50% homology to at least one of SEQ ID NO:2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;  
sequences complementary to SEQ ID NO:2; and  
sequences complementary to variants having at least about 50% homology to SEQ ID NO:2 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and  
polypeptides having at least 10 consecutive amino acids of a polypeptide having a sequence selected from the group consisting of SEQ ID NO:2; and  
wherein the protein preparation is a liquid.

94. A protein preparation comprising a polypeptide selected from the group consisting of:  
polypeptides having an amino acid sequence selected from the group consisting of:

SEQ ID NO:2;  
variants having at least about 50% homology to at least one of SEQ ID NO:2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;  
sequences complementary to SEQ ID NO:2; and  
sequences complementary to variants having at least about 50% homology to SEQ ID NO:2 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and  
polypeptides having at least 10 consecutive amino acids of a polypeptide having a sequence selected from the group consisting of SEQ ID NO:2; and  
wherein the polypeptide is a solid.

95. A method for modifying small molecules, comprising the step of mixing at least one polypeptide encoded by a polynucleotide selected from the group consisting of:

SEQ ID NO:1;

variants having at least about 50% homology to at least one of SEQ ID NO:1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;

sequences complementary to SEQ ID NO:1; and

sequences complementary to variants having at least about 50% homology to SEQ ID NO:1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and fragments of any of the foregoing polypeptides;

with at least one small molecule to produce at least one modified small molecule via at least one biocatalytic reaction, wherein the at least one polypeptide has alpha amylase activity.

96. The method of claim 95, wherein the at least one polypeptide comprises a plurality of polypeptides and the at least one small molecule comprises a plurality of small molecules, whereby a plurality of modified small molecules are produced via a plurality of biocatalytic reactions to form a library of modified small molecules.

97. The method of 96, further comprising the step of testing the library to determine if a particular modified small molecule, which exhibits a desired activity is present within the library.

98. The method of claim 97 wherein the step of testing the library further comprises the steps of: systematically eliminating all but one of the biocatalytic reactions used to produce a portion of the plurality of the modified small molecules within the library by testing the portion of the modified small molecule for the presence or absence of the particular modified small molecule with the desired activity, and identifying a specific biocatalytic reaction which produces the particular modified small molecule of desired activity.

99. The method of claim 98 wherein the specific biocatalytic reaction, which produces the modified small molecule of desired activity is repeated.

100. The method of claim 93 wherein the biocatalytic reactions are conducted with a group of biocatalysts that react with distinct structural moieties found within the at least one small molecule;

each biocatalyst is specific for a particular structural moiety or a group of related structural moieties; and

each biocatalyst reacts with a plurality of small molecules which contain the particular structural moiety specific to the particular biocatalyst.

101. A cloning vector comprising a sequence that encodes a polypeptide having alpha amylase activity, said sequence being selected from the group consisting of:

SEQ ID NO:1;

variants having at least about 50% homology to at least one of SEQ ID NO:1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;

sequences complementary to SEQ ID NO:1; and

sequences complementary to variants having at least about 50% homology to SEQ ID NO:1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection.

102. A host cell comprising a sequence that encodes a polypeptide having alpha amylase activity, said sequence being selected from the group consisting of:

SEQ ID NO:1;

variants having at least about 50% homology to at least one of SEQ ID NO:1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection;

sequences complementary to SEQ ID NO:1; and

sequences complementary to variants having at least about 50% homology to SEQ ID NO:1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection.

104. A vector as claimed in claim 101 or 103, wherein the vector is selected from the group consisting of viral vectors, plasmid vectors, phage vectors, phagemid vectors, cosmids, fosmids, bacteriophages, artificial chromosomes, adenovirus vectors, retroviral vectors, and adeno-associated viral vectors.

105. A host cell comprising an expression vector as claimed in claim 103.

106. A host cell as claimed in claim 47, 102, 103 or 105, wherein the host is selected from the group consisting of prokaryotes, eukaryotes, fungi, yeasts, plants and metabolically rich hosts.

107. A method for liquefying a starch containing composition comprising contacting the starch with a polypeptide of claim 30.

108. A liquefied syrup produced by the method of claim 107.

109. A liquified syrup having the oligosaccharide profile of the syrup of claim 108.

110. A liquefied syrup having the NN/MW ratio of less than about 2.0 at 18 DE and less than about 4.0 at 12 DE.

111. A method for washing an object comprising contacting said object with a polypeptide of claim 30 under conditions sufficient for said washing.
112. A method for textile desizing comprising contacting said textile with a polypeptide of claim 30 under conditions sufficient for said desizing.
113. A method for the treatment of lignocellulosic fibers, wherein the fibers are treated with a polypeptide of claim 30, in an amount which is efficient for improving the fiber properties.
114. A method according to claim 113 for enzymatic deinking of recycled paper pulp, wherein the polypeptide of claim 30 is applied in an amount which is efficient for effective deinking of the fiber surface.
115. A method for starch liquefaction comprising contacting said starch with with a polypeptide of claim 30 under conditions sufficient for said liquefaction.
116. A detergent additive comprising with a polypeptide of claim 30.
117. A method as in any of claims 107-116, wherein the polypeptide is set forth in SEQ ID NO:2, or functional variants thereof.
118. A method for producing a high-maltose or a high-glucose syrup or a mixed syrup comprising:  
liquefying starch using an effective amount of a polypeptide of claim 30 to obtain a soluble starch hydrolysate; and  
saccharifying the soluble starch hydrolysate, thereby resulting in a syrup.
119. The method as in any of claims 107, 115, or 118, wherein the starch is from a material selected from rice, germinated rice, corn, barley, wheat, legumes and sweet potato.

120. The method as in any of claims 107, 115, or 118, further comprising addition of a second alpha amylase or a beta amylase or a combination thereof.

121. A method of increasing the flow of production fluids from a subterranean formation by removing a viscous, starch-containing, damaging fluid formed during production operations and found within the subterranean formation which surrounds a completed well bore comprising:

- allowing production fluids to flow from the well bore;
- reducing the flow of production fluids from the formation below expected flow rates;
- formulating an enzyme treatment by blending together an aqueous fluid and a polypeptide of claim 30;
- pumping the enzyme treatment to a desired location within the well bore;
- allowing the enzyme treatment to degrade the viscous, starch-containing, damaging fluid,

whereby the fluid can be removed from the subterranean formation to the well surface; and

- wherein the enzyme treatment is effective to attack the alpha glucosidic linkages in the starch-containing fluid.

122. The method of claim 121, wherein the enzyme is set forth in SEQ ID NO:2.